

Application No. 10/763,502
Response dated August 15, 2007, 2007
Reply to March 15, 2007 Office Action

Exhibit A



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

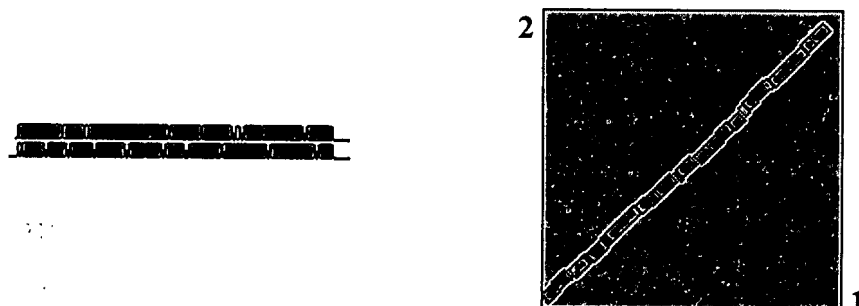
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **0** expect: **10.0000** wordsize: **3** Filter ☒ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1(C. elegans PAMP - SEQ ID NO:12)
 Length = 720 (1 .. 720)

Sequence 2: lcl|seq_2(Mouse PAMP - SEQ ID NO:16)
 Length = 708 (1 .. 708)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Sequence 1: lcl|seq_1(C. elegans PAMP - SEQ ID NO:12)
 Sequence 2: lcl|seq_2(Mouse PAMP - SEQ ID NO:16)

Score = 160 bits (405), Expect = 5e-37

Identities = 154/701 (21%), Positives = 291/701 (41%), Gaps = 83/701 (11%)

| | | | |
|-------|-----|---|-----|
| Query | 9 | LIAGIRCDGFSQVFRTLFIGEGNACYRTFNKTHEFGCQANRENENGLIVRIDKQEDFK | 68 |
| | | +++AG+ C G S + + + + C R N TH+ GCQ++ + G+I ++K+ED K | |
| Sbjct | 24 | VVLAGL-CGGNSVERKIYIPLNKTAPCVRLNATHQIGCQSSISGDTGVIHVVEKEEDLK | 82 |
| Query | 69 | NLDSCWNSFYPKYSGKYWALLPVNLIRRDITISQLKSSKC-LSGIVLYNSGESIHPGDEST | 127 |
| | | W + Y LL L RD + +LK + ++G+ + ++ + ++ | |
| Sbjct | 83 | -----W-VLTDGPNPPYMLLEGKLFTRDVMELKGTTSRIAGLAV-----TLAKPNSTS | 131 |
| Query | 128 | AASHDAECPNAASDYLLQDKNEEY--CERKI-NSRGAITRDGLMKIDWRIQMVFIDNSTD | 184 |
| | | + S +CPN Y E+ C++ + N G +GL D+ + +++ + | |
| Sbjct | 132 | SFSPSVQCPNDGFGIYSNSYGPEFAHCKKTLWNLG---NGLAYEDFSFPIFILLEDENE | 187 |
| Query | 185 | LEIIEKCYSMFNKPKEDGSSGYPCGMSFRLANMAAGNSEICYRRGKNDAKLFQMNIDSG | 244 |
| | | ++I++CY N + + +P C M A ++ C RR F + S | |
| Sbjct | 188 | TKVIKQCYQDHNLGQNGSAPSFLCAMQLFSHMHAVISTATCMRRS-----FIQSTFSI | 241 |

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Query  245  DAPQLCGAMHSDNIFAFPTPIPTSPNETIITSKYMMVTARMDSFSGMPEISVGEVSVLT  304
          +   +C   +   N+++   PI TS   E   +   +   ++   R+DS   ++ G   S   +
Sbjct  242  NPEIVCDPLSDYNVWSMLKPINTSVGLEPDV--RVVVAATRLDSRSFFWNVAPGAESAVA  299

Query  305  SIISVLAAARSMGTQIEKWQKASN--TSNRNVFFAFFNGESLDYIGSGAAAYQMENGKFP  362
          S ++ LAAA ++           KA +   T +RNV F FF GE+ DYIGS   Y MENGKF
Sbjct  300  SFVTQLAAAEAL-----HKAPDVTTLSRNVMFVFFQGETFDYIGSSRMVYDMENGKF-  351

Query  363  QMIRSDRTHIHPIRPNELDYILEVQQIGVAKGRKYYVHVD--GERYQQNKQTQDRVIDRI  420
          P+R   +D   +E+ Q+ +           ++H D   ++ +   K Q + ++ +
Sbjct  352  -----PVRLNIDSFVELGQVALRTSLDLWMHTDPM SQKNESVKNQVEDLLATL  400

Query  421  ERGLRSHAFDLEKPSGSGDRVPPASWHSFAKADAHVQSVLLAPYGKEYEYQRVNSILDK-  479
          E+           + +           +PP+S   F +A   ++ V+LA +   + +   SI D
Sbjct  401  EKSGAGVPEVVLRRLAQS QALPPSSLQRFLRA-RNISGVVLADHSGSFHNRYQSIYDTA  459

Query  480  -----NEWTEDERE-----KAIQEIEAVSTAILAAAADYVGVETDEVVAKVDKKLITT  527
          EW   E +           + + V+T +   A   +   G           + D + +T
Sbjct  460  ENINVTYPEWQSPEEDLNFVTD TAKALANVATVLARALYELAGGTNFSSSIQADPQTVTR  519

Query  528  IFDCLI--TSNFWFDCDFMQKLDGGRYHKLFN SYGFNQKSTYISMESHTAFPTVLHWLTI  585
          +   +   +N WF           H L +           YI++ S T   V+ +
Sbjct  520  LLYGFLVKANNSWFQSILK-----HDLRSYDDRPLQHYIAVSSPTNTTYVVQYALA  571

Query  586  FALGSDKETLNVKSEKSCSHLGQFQAMYTYTWQPNPYTGNFS-----CLKSAIVKKVMVS  640
          G           + +           + + +Y Y+W   P+   N +           C++S +   +S
Sbjct  572  NLTGKATNLTREQCQDPSKVPNESKDLYEYSWVQGPWNSNRTERLPQCVRSTVRLARALS  631

Query  641  PAVDSQTPEEEMNTRYSTWMESVYIIESVNLYLMEDASF EY  681
          PA +           +   +T YSTW ES +           ++L+           E+
Sbjct  632  PAFEL---SQWSSTEYSTWAESRWKDIQARIFLIASKKLEF  669

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CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.



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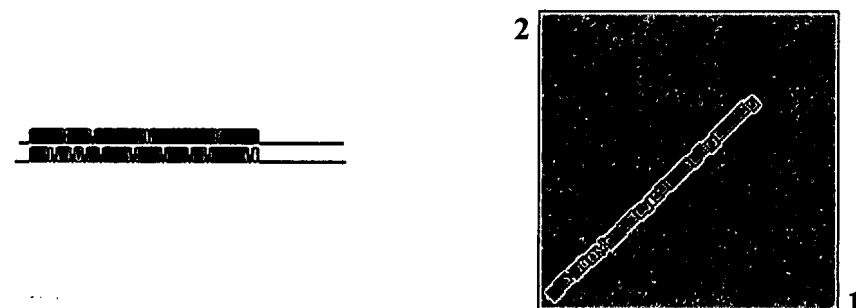
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☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1(C. elegans PAMP - SEQ ID NO:12)
 Length = 720 (1 .. 720)

Sequence 2: lcl|seq_2(D. melanogaster PAMP - SEQ ID NO:18)
 Length = 695 (1 .. 695)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 115 bits (288), Expect = 2e-23
 Identities = 116/501 (23%), Positives = 210/501 (41%), Gaps = 62/501 (12%)

| | | | |
|-------|-----|---|-----|
| Query | 32 | GNACYRTFNKTHEFGCQANRENENGLIVRIDKQEDFKNLDSCWNSFYPKYSGKYWALLPV | 91 |
| | | G +C+R N TH+ GC + G++ I+ + D + L S S P Y+ ++P | |
| Sbjct | 37 | GASCFRRLNGTHQTGCSSTYSGSVGLHLINVEADLEFLLSSPPS--PPYA----PMIPP | 90 |
| Query | 92 | NLIRRDITISQLKSS--KCLSGIVLYNSGESIHGDESTAASHDAECPNAASDYLLQDKNE | 149 |
| | | +L R+ + +LK + K +S ++L N ++ SH+ CPN S + | |
| Sbjct | 91 | HLFTRNNLMRLKEAGPKNISVLLINRT-----NQMKQFSHELNCNPQYSGL---NSTS | 141 |
| Query | 150 | EYCE-----RKINSRGAITRDGLMKIDWRIQMVFIDNSTDLEIIEKCYSMFNKPKEDGSS | 204 |
| | | E C+ + N G GL+ D+ + +I + + +EKC+ FN + + | |
| Sbjct | 142 | ETCDASNPAKNWNPWGT----GLLHEDFFPIYYIADLDQVTKLEKCFQDFNNHNYETHA | 197 |
| Query | 205 | GYPYCGMSFRLANMAAGNSEICYRRGKNDAKLFQMNIIDSGDAPQLCGAMHSDNIFAFPTP | 264 |
| | | C + + AA N+E+C RR I++ + C + N+ TP | |
| Sbjct | 198 | LRSLCAVEVKSFMSAAVNTEVCMRRTNF-----INNLGGSKYCDPLEGRNVSPPTP | 249 |

Query 265 IP--TSPTNETIITS-KYMMVTARMDSFSGMPEISVGEVSVLTSIISVLAAARSMGTQIE 321
+ T ET+ T+ K+++VT R+D+ M + +G + L A + ++
Sbjct 250 ESQQSETTLETVHTNEKFILVTCRLDTTTFDGVGLGAMDSLGMF---AVFTHVAYLLK 305

Query 322 KWQKASNTSNRNVFFAFFNGESLDYIGSGAAAYQMENGKFPQMIRSDRTHIHPIRPNELD 381
+ + NV F FNGES DYIGS Y ME +FP ++ T PI + +D
Sbjct 306 QLLPPQSKDLHNVLFVTFNGESYDYIGSQRFVYDMEKLQFP---TESTGTPPIAFDNID 361

Query 382 YILEVQQIGVAKGRKYYVHVDGERYQQNKTQTDRVIDRIERGLRS--HAFDLEKPSGSGD 439
++L++ + K + T ++++R+ +S + F+L S
Sbjct 362 FMLDIGTLDDISNIKLHA-----LNGTTLAQQILERLNNYAKSPRYGFNLNIQSEMSA 414

Query 440 RVPPASWHSFAKADAHVQSVLLAPYGKEYEYQRVNSILDKNEWTEDEREKAIQEIEAVST 499
+PP S SF + D + +++L Y D ++T K ++ V+
Sbjct 415 HLPPTSAQSFLRRDPNFNALILNARPTNKYYHSTYDDADNVDFTYANTSKDFTQLTEVN- 473

Query 500 AILAAAADYVGVETDEVVAKV 520
D+ + D + KV
Sbjct 474 -----DFKSLNPDSLQMKV 487

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.